



PATENT  
ATTORNEY DOCKET NO. A21-535.1007  
07148/032001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Lorin R. DeBonte et al.                      Art Unit: 1649  
Serial No.: 08/572,027                                      Examiner: G. Benzion  
Filed : December, 14, 1995  
Title : PLANTS HAVING MUTANT SEQUENCES THAT CONFER ALTERED  
FATTY ACID PROFILES

Assistant Commissioner for Patents  
Washington, DC 20231

DECLARATION UNDER 37 CFR §1.132 OF GUO-HUA MIAO

I, Guo-Hua Miao, declare as follows:

1. That I am a citizen of the People's Republic of China and presently live at 202 Cherry Blossom Place, Hockessin, Delaware.
2. That I received a Bachelor of Science degree in Biology from Shanghai Normal University, Shanghai, China in 1982, a Master of Science degree in Plant Physiology from Shanghai Institute of Plant Physiology, Chinese Academy of Science, Shanghai, China in 1984 and a Doctor of Philosophy degree in Molecular, Cellular and Developmental Biology from Ohio State University, Columbus, Ohio in 1991.
3. That I was employed as a research associate at the Biotechnology Center, Ohio State University, Columbus, Ohio from 1991 to 1993.
4. That I am presently employed as a Senior Research Molecular Biologist by DuPont Agricultural Products, a division of E. I. Dupont de Nemours, Inc. and have been so employed since 1993.
5. That, as an employee of DuPont, I determined Fad2 desaturase coding sequences obtained from canola lines Westar and Q508. Westar is a canola variety having no known mutations in

Declaration of Guo-Hau Miao  
Serial No. 08/572,027

Fad2 desaturase genes. Q508 is a line derived from Westar by mutagenesis. A copy of four microfilmed pages from my laboratory notebook is attached as Exhibit A (Notebook F79066, pages 140-143). These notebook pages show the DNA sequences and deduced amino acid sequences that were obtained by me or under my supervision. The dates on these four pages, all of which are prior to December 14, 1995, have been blocked out.

The DNA and deduced amino acid sequence of Fad2-F from line Q508 is shown at pages 140-141. The Q508 Fad2-F sequence contains a mutation at nucleotide 515 compared to the wild-type Westar sequence, as indicated at page 140 of the notebook. The wild-type nucleotide at this position is T, and the mutant nucleotide is A. Based on the information at pages 140-141, the mutant Q508 Fad2-F and wild-type Fad2-F sequences contain a G at position 316.

The DNA and deduced amino acid sequences of Fad2-D from the Westar variety is shown at pages 142-143. The wild-type Fad2-D sequence contains a G at nucleotide 316, whereas the IMC 129 mutant Fad2-D sequence contains an A, as indicated at page 142 of the notebook. Based on the information at pages 142-143, the wild-type Fad2-D and mutant IMC 129 Fad2-D sequences contain a T at position 515.

6. After these sequences were determined, the mutant Fad2-D sequence and the mutant Fad2-F sequence were mailed to Ronald Lundquist. A copy of the sequences that were mailed, as well as the cover letter, are attached hereto as Exhibit B. The dates on these pages, all of which are prior to December 14, 1995, have been blocked out. A comparison of the nucleotide sequences in my laboratory notebook to those enclosed with the letter to Ronald Lundquist indicates that the sequences enclosed in the letter were incorrectly labeled. The sequence labeled as "f-gene, 508" corresponds to the wild-type Fad2-D sequence of my

Declaration of Guo-Hau Miao  
Serial No. 08/572,027

notebook, with the Q508 mutation inserted at position 515. The sequence labeled as "d-gene, 129" corresponds to the wild-type Fad2-F sequence of my notebook, with the IMC 129 mutation inserted at position 316. It appears that the sequence labels were inadvertently switched and the D and F mutations added to the sequence prior to mailing the information to Mr. Lundquist.

7. I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the instant patent application or any patent issuing thereon.

Dated: 7/1/95

Guo-Hua Miao, Ph.D.

14066.M11

## 140

Page No.

**TITLE**

Cont'd from Pg 157

DATE \_\_\_\_\_

**E 79066**

Book No. \_\_\_\_\_

## PURPOSE

cont'd from page 137

DNA and deduced  
protein sequence  
of canine FOD2  
(p) from Q58.

CTC was found  
in water and  
12.9 clays.

~~Fluss in Guss~~

a thistle ~~was~~  
replaces leucine  
position 514-516

this mutation

~~Q~~ in Dec

i) specific to

(b)(7)(C)

42508

Sequence in this

Resin W43

confirmed from both strands

## EXPERIMENTER

DATE \_\_\_\_\_

WITNESSED BY

DATE \_\_\_\_\_

TITLE

*cont'd*

DATE

Page No.

141

PURPOSE

*cont'd*

Book No.

E 79066

625 630 635 640 645 650 655 660 665 670  
TCC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC  
ACG GTA AAG GTG GGG ITG CGA GCG TAG ATG TTG CTG GCG CTC GCA GAG  
C H F H P N A P I Y N D R E R L  
675 680 685 690 695 700 705 710 715 720  
CAG ATA TAC ATC TCC GAC GCT GCG ATC CTC GCG GTC TGC TAC GGT CTC  
GTC TAT ATG TAG AGC CTC CGA CCG TAG GAG CCG CAG ACG ATG CCA GAG  
Q I Y I S D A G I L A V C Y G L  
725 730 735 740 745 750 755 760 765  
TTC CGT TAC CCG GCG GCG CAG GGA GTG GCG TCG ATG GTC TCC TTC TAC  
AAG GCA ATG CCG GCG GCG CTC CCT CAC CCG AGC TAC CAG ACG AAG ATG  
F R Y A A G Q G V A S M V C F Y  
770 775 780 785 790 795 800 805 810 815  
GGA GTC CCG CTT CTG ATT GTC AAT GGT TTC CTC GTG TTG ATC ACT TAC  
CCT CAG GCG GAA GAC TAA CAG TTA CCA AAG GAG CAC AAC TAG TGA ATG  
G V P L L I V N G F L V L I T Y  
820 825 830 835 840 845 850 855 860  
TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG  
AAC GTC GTG TGC GTA GGA AGG GAC GGA GTG ATG CTA ACG AGG CTC ACC  
L Q H T H P S L P H Y D S S E W  
865 870 875 880 885 890 895 900 905 910  
GAT TGG TTC AGG GGA GGT ITG GCT ACC GTT GAC AGA GAC TAC GGA ATC  
CTA ACC AAG TCC CCT CGA AAC CGA TGG CAA CTG TCT CTG ATG CCT TAG  
D M F R G A L A T V D R D Y G I  
915 920 925 930 935 940 945 950 955 960  
TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCG CAT CAT  
AAC ITG TTC CAG AAG GTG TTA TAA TGG CTG TCG GTC CAC CCG GTA GTA  
L N K V F H N I T D T H V A H H  
965 970 975 980 985 990 995 1000 1005  
CGG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GGT ACC AAG GCG  
GCG AAG ACG TGC TAC GCG GTA ATA GTG CCG TAC CTT CGA TGG TTC CCG  
P F S T M P H Y H A M E A T R A  
1010 1015 1020 1025 1030 1035 1040 1045 1050 1055  
ATA AAG CCG ATA CTG GGA CAC TAT TAT CAC TTC GAT GCG ACG CCG GTG  
TAT TTC GCG TAT GAC CCT CTC ATA ATA GTG AAG CTA CCG TCG GCG CAC  
I K P I L G E Y Y Q F D G T P V  
1060 1065 1070 1075 1080 1085 1090 1095 1100  
GTT AAG CCG ATC TCG AGG GAG CCG AAG CAC TGT ATC TAT CTG GAA CCG  
CAA TTC CCG TAC ACG TCC CTC CCG TTC CTC ACA TAG ATA CAC CTT GCG  
V K A M W R E A K E C I Y V E P  
1105 1110 1115 1120 1125 1130 1135 1140 1145 1150  
CAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA  
CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACG ATG TTC TTA TTC AAT  
D R Q G E K K G V F W Y N N K L  
1155 1160 1165 1170 1175 1180 1185  
TGA GCA TAT GAT GAT GGT GAA AGA AAT CAC TAG  
ACT CCT ATA CTA CTA CCA CTT TCT TTA GTG ATC  
C Y D D G E R N H

See prime location

in page 134

In Q508

a MAI S.L

was last kind

on the sequence

analysis

CCTC (CCTC)

CCAC (CCTC)

MAI S.L (CCTC)

Therefore, MAI

will provide a

simple way to

disguish Q508

and WC + 129

EXPERIMENTER

*Smith*

DATE

WITNESSED BY

*CH*

DATE

## E. I. DUPONT DE NEMOURS AND COMPANY

142

Page No. TITLE

DATE

E 79066

Book No. PURPOSE

5 10 15 20 25 30 35 40 45  
 ATG GGT GCA GGT GGA AGA ATG CAA GTG TGT CCT CCC TCC AAA AAG TCT  
 TAC CCA CGT CCA CTT TCT TAC GTT CAC AGA GGA GGG AGG TTT TTC AGA  
 M G A G G R M Q V S P P S K K S>  
 50 55 60 65 70 75 80 85 90 95  
 GAA ACC GAC AAC ATC AAG CCG GTA CCG TGC GAG ACA CCG CCC TTC ACT  
 CTT TGG CTG TTG TAG TTC GCG CAT GGG ACC CTC TGT GGC GGG AAG TGA  
 E T D N I K R V P C E T P P P P T>  
 100 105 110 115 120 125 130 135 140  
 CTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CCG TCG  
 CAG CTT GTT GAG TTC TTT CTT TAG GGT GGC GTG ACA AAG TTT GCG AGC  
 V G E L K K A I P P H C F K R S>  
 145 150 155 160 165 170 175 180 185 190  
 ATC CTT CCG TGT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCG  
 TAG GGA GCG AGA AAG AGG ATG GAG TAG ACC CTG TAG TAG TAT CCG AGG  
 I P R S F S Y L I W D I I I A S>  
 195 200 205 210 215 220 225 230 235 240  
 ATG TTC TAC TAC GTC GCG ACC ACT TAC TTC CTT CTC CTC CTT CAC CTT  
 ACG AAG ATG ATG CAG CCG TGG TGA ATG AAG GGA GAG GAG GGA GTG GGA  
 C F Y Y V A T T Y F P L L P H P>  
 245 250 255 260 265 270 275 280 285  
 CTC TCC TAC TTC GCG TCG CTT CTC TAC TGG GCG TGC CAG GCG TCC GTC  
 GAG AGG ATG AAG ACC AGG GGA GAG ATG ACC CCG AGG GTC CCG ACC CAG  
 L S Y F A W P L Y W A C  
 290 295 300 305 310 315 320 325 330 335  
 CTA ACC GCG GTC TGG GTC ATA GCG CAC GAG TGC GGC CAG CAC GCG TTC  
 GAT TCG CCG CAG ACC CAG TAT CCG GTG CTC ACG CCG GTG GTG CCG AAG  
 340 345 350 355 360 365 370 375 380  
 AGC GAC TAC CAC TGG CTG GAC GAC ACC GTC GCG CTC ATC TTC CAC TCC  
 TCG CTG ATG CCG ACC CAG CTG CTG TGG CAG CCG CAG TAG AAG GTG AGG  
 385 390 395 400 405 410 415 420 425 430  
 TTC CTC CTC GTC CTT TAC TTC TCC TGG AAG TAC AGT CAT CGA CCG CAC  
 AAG GAG GAG CAG AGA ATG AAG ACC TTC ATG TGA GTA GGT CCG GTG  
 F L L V P Y F S W K Y S H R R H>  
 435 440 445 450 455 460 465 470 475 480  
 CAT TCC AAC ACT GCG TCC CTC GAG AGA GAC GAA GTG TTT GTC CCG AAG  
 GTA AGG TTG TGA CCG AGG GAG CTC TCT CTG CTT CAC AAA CAG GGG TTC  
 H S N I G S L E R D E V F V P R>  
 485 490 495 500 505 510 515 520 525  
 AAG AAG TCA GAC ATC AAG TGG TAC GCG AAG TAC CTC AAC AAC CTT TTG  
 TTC TTC AGT CTG TAG TTC ACC ATC CCG TTC ATG GAG TTG TTG GGA AAC  
 K K S D I K W Y G K Y L N N P L>  
 530 535 540 545 550 555 560 565 570 575  
 GGA CCG ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GCG TGG CTT TTG  
 CTT CCG TGC CAC TAC AAT TGC CAA GAG TGA GAG CCG ACC GGA AAC  
 G R T V M L T V Q F T L G W P L>  
 580 585 590 595 600 605 610 615 620  
 TAC TTA GCG TTC AAC GTC TCG GCG AGA CTT TAC CAC GCG CCG TTC GCT  
 ATC AAT CCG AAG TTG CAG ACC CCG TCT GGA ATG CTC CCG CCG AAG CGA  
 Y L A F B V S G R P Y D G G F A>

DNB and deduced  
 protein sequence  
 from vector FAD2  
 (B) clone

In 129 and  
 Q508 clones  
 (E)  
 CAG was converted  
 to AAG (K)

This mutation  
 was found in  
 F clone only.

but occur

In both 129 and  
 Q508 mutant  
 lines

Again, this  
 region was  
 confirmed from

EXPERIMENTER

E. I. Dupont

DATE

WITNESSED BY

E. I. Dupont

DATE

TITLE

*cont'd*

DATE

Page No.

143

PURPOSE

*cont'd*

Book No. E 79066

625 630 635 640 645 650 655 660 665 670  
 TCC CAT TTC CAC CCC AAC GCT CCG ATC TAC AAC GAC CGC GAG CGT CTC  
 ACC GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG GCG GTC GCA CAG  
 C H F H P N A P I Y N D R E R L>  
 675 680 685 690 695 700 705 710 715 720  
 CAG ATA TAC ATC TCC GAC GCT GCG ATC CTC GCG GTC TAC TAC GCT CTC  
 GTC TAT ATG TAG AGG CTG CGA CCG TAC CAG CCG CAG ACC ATG CCA CAG  
 Q I Y I S D A C I L A V C T G L>  
 725 730 735 740 745 750 755 760 765  
 TAC CGC TAC GCT GCT GTC CAA GGA GTT GCG TCG ATG GTC TCC TTC TAC  
 ATG CGC ATG CGA CGA CAG GTT CCT CAA CCG AGC TAC CAG ACC AAG ATG  
 Y R Y A A V Q G V A S M V C F Y>  
 770 775 780 785 790 795 800 805 810 815  
 GGA GTT CCG CTT CTG ATT GTC AAT GGG TTC TTA GTT TTG ATC ACT TAC  
 CCT CAA GCG GAA GAC TAA CAG TTA CCG AAG AAT CAA AAC TAG TGA ATG  
 G V P L L I V N G F L V L I T Y>  
 820 825 830 835 840 845 850 855 860  
 TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG TCT GAG TCG  
 AAC CTG GTG TGC GTA GGA AGG GAC GGA GTG ATA CTG AGC AGA CTC ACC  
 L Q H T H P S L P H Y D S S E W>  
 865 870 875 880 885 890 895 900 905 910  
 CAT TGG TTG AGG GGA GCT TTG GCG ACC GTT CAC AGA GAC TAC GGA ATC  
 CTA ACC AAC TCC CCG CGA AAG CCG TCC CAA TCG TCT CTC ATG CCT TAG  
 D W L R G A L A T V D R D Y G I>  
 915 920 925 930 935 940 945 950 955 960  
 TTG AAC AAG GTC TTC CAC AAT ATC ACC GAC ACG CAC GTG GCG CAT CAC  
 AAC TTG TTC CAG AAG GTG TTA TAG TCC CTG TCC GTG CAC CCG GTA GTG  
 L N K V F H N I T D T H V A H H>  
 965 970 975 980 985 990 995 1000 1005  
 CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT ACG AAG CCG  
 GAC AAG AGC TGG TAC GCG GTA ATA GTA CCG TAC CTT CGA TCG TTC CCG  
 L F S T M P H Y H A M E A T K A>  
 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055  
 ATA AAG CCG ATA CTG CGA GAG TAT TAT CAG TTG CAT GCG ACC CCG GTG  
 TAT TTC GCG TAT CAC CCT CTC ATA ATA GTC AAC GTA CCG TCG GCG CAC  
 I K P I L G E Y Y Q L H G T P V>  
 1060 1065 1070 1075 1080 1085 1090 1095 1100  
 GTT AAG CCG ATG TCG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG  
 CAA TTC CCG TAC ACC TCG CTC CCG TTC CTC ACA TAG ATA CAC CTT GCG  
 V K A M W R E A K E C I Y V E P>  
 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150  
 CAC AGG CAA GGT GAG AAG AAA GGT CTC TTC TGG TAC AAC AAT AAG TTA  
 CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT  
 D R Q G E K K G V F W Y N N X L>  
 1155 1160 1165 1170  
 TCA AGC AAA GAA GAA ACA AT  
 ACT TCC TTT CTT CTT TGT TA  
 S K E E T X

*both strands**(see page 134)**for primer location**Total 5 indels**129 and 9508**clones (each with)**5' and 3' ends**Sequence by**primer DR**(see page 134)**and showed the**same mutation**Thus it appears**to be true**mutation**This will be**further confirmed**by re RT-PCR**RNA from 129 and 9508**and sequenced by**DR primer*

EXPERIMENTER

*George A. Hill*

DATE

WITNESSED BY

*C. Shoppard*

DATE



AGRICULTURAL PRODUCTS  
Experimental Station  
P.O. Box 80402  
Wilmington, Delaware 19880-0402

RECEIVED

RONALD C. LUNDQUIST

Mr. Ronald Lundquist  
Fisher Richardson  
330 Dain Bosworth Tower  
60 S. 6th St.  
Minneapolis, Minnesota 55402

Dear Ron:

It was very nice speaking with you over the phone on Monday. I am sending you the information about the molecular analysis of IMC129 and IMCQ508 mutations, which you requested for IMC129 and IMCQ508 patent application. A disc containing the nucleotide sequences for both canola FAD2 genes (D and F) are also included.

As we discussed over the phone, IMCQ508 mutation was identified based on sequencing of cDNA clones isolated from IMCQ508 mutant, however, the mutation had not been confirmed as we did for IMC129 mutation. Therefore, we might need to further confirm the mutation, if we would like to include IMCQ508 in the patent application. Please feel free to contact me if I can provide you any additional information about the two mutants.

Sincerely,

Guo-Hua Miao, Ph.D.  
Research Molecular Biologist

CC: W. R. Majarian

Encl.



```

      5    10    15    20    25    30    35    40    45    50
      *      *      *      *      *      *      *      *
ATGGGTGCAG GTGGAAGAAT GCAAGTGTCT CCTCCCTCCA AAAAGTCTGA
TACCCACGTC CACCTTCTTA CGTTCACAGA GGAGGGAGGT TTTTCAGACT

     55    60    65    70    75    80    85    90    95   100
     *      *      *      *      *      *      *      *
AACCGACAAC ATCAAGCGCG TACCCTGCGA GACACCGCCC TTCACTGTCTG
TTGGCTGTGTG TAGTTCGCGC ATGGGACGCT CTGTGGCGGG AAGTGACAGC

    105   110   115   120   125   130   135   140   145   150
     *      *      *      *      *      *      *      *
GAGAACTCAA GAAAGCAATC CCACCGCACT GTTTCAAACG CTCGATCCCT
CTCTTGAGTT CTTTCGTTAG GGTGGCGTGA CAAAGTTTGC GAGCTAGGGA

    155   160   165   170   175   180   185   190   195   200
     *      *      *      *      *      *      *      *
CGCTCTTTCT CCTACCTCAT CTGGGACATC ATCATAGCCT CCTGCTTCTA
GCGAGAAAGA GGATGGAGTA GACCCTGTAG TAGTATCGGA GGACGAAGAT

    205   210   215   220   225   230   235   240   245   250
     *      *      *      *      *      *      *      *
CTACGTCGCC ACCACTTACT TCCCTCTCCT CCCTCACCTT CTCTCCTACT
GATGCAGCGG TGGTGAATGA AGGGAGAGGA GGGAGTGGGA GAGAGGATGA

    255   260   265   270   275   280   285   290   295   300
     *      *      *      *      *      *      *      *
TCGCCTGGCC TCTCTACTGG GCCTGCCAGG GCTGCGTCCT AACCGGCGTC
AGCGGACCGG AGAGATGACC CGGACGGTCC CGACGCAGGA TTGGCCGCGA

    305   310   315   320   325   330   335   340   345   350
     *      *      *      *      *      *      *      *
TGGGTCATAG CCCACAGTGT CGGCCACCAC GCCTTCAGCG ACTACCAGTG
ACCCAGTATC GGGTGTTCAC GCCGGTGGTG CGGAAGTCGC TGATGGTCAC

    355   360   365   370   375   380   385   390   395   400
     *      *      *      *      *      *      *      *
GCTGGACGAC ACCGTCGGCC TCATCTTCCA CTCCTTCCTC CTCGTCCCTT
CGACCTGCTG TGGCAGCCGG AGTAGAAGGT GAGGAAGGAG GAGCAGGGAA

    405   410   415   420   425   430   435   440   445   450
     *      *      *      *      *      *      *      *
ACTTCTCCTG GAAGTACAGT CATCGACGCC ACCATTCCAA CACTGGCTCC
TGAAGAGGAC CTTTCATGTCA GTAGCTGCGG TGGTAAGGTT GTGACCGAGG

    455   460   465   470   475   480   485   490   495   500
     *      *      *      *      *      *      *      *
CTCGAGAGAG ACGAAGTGTT TGTCCCCAAG AAGAAGTCAG ACATCAAGTG
GAGCTCTCTC TGCTTCACAA ACAGGGGTTC TTCTTCAGTC TGTAGTTTAC

    505   510   515   520   525   530   535   540   545   550
     *      *      *      *      *      *      *      *
GTACGGCAAG TACCAACAAC ACCCTTTGGG ACGCACCGTG ATGTTAACGG
CATGCCGTTT ATGGTGTGTG TGGGAAACCC TGGCTGGCAC TACAATTGCC

    555   560   565   570   575   580   585   590   595   600
     *      *      *      *      *      *      *      *
TTCAGTTTAC TCTCGGCTGG CCTTTGTACT TAGCCTTCAA CGTCTCGGGG
AAGTCAAGTG AGAGCCGACC GGAAACATGA ATCGGAAGTT GCAGAGCCCC

    605   610   615   620   625   630   635   640   645   650
     *      *      *      *      *      *      *      *
AGACCTTACG ACGGCGGCTT CGCTTGCCAT TTCCACCCCA ACGCTCCCAT

```

```

TCTGGAATGC TGCCGCCGAA GCGAACGGTA AAGGTGGGGT TGCGAGGGTA
    655 660      665 670      675 680      685 690      695 700
          *              *              *              *
CTACAACGAC CGCGAGCGTC TCCAGATATA CATCTCCGAC GCTGGCATCC
GATGTTGCTG GCGCTCGCAG AGGTCTATAT GTAGAGGCTG CGACCGTAGG

    705 710      715 720      725 730      735 740      745 750
          *              *              *              *
TCGCCGTCTG CTACGGTCTC TACCGCTACG CTGCTGTCCA AGGAGTTGCC
ACGGGCAGAC GATGCCAGAG ATGGCGATGC GACGACAGGT TCCTCAACGG

    755 760      765 770      775 780      785 790      795 800
          *              *              *              *
TCGATGGTCT GCTTCTACGG AGTTCCGCTT CTGATTGTCA ATGGGTTCTT
AGCTACCAGA CGAAGATGCC TCAAGGCGAA GACTAACAGT TACCCAAGAA

    805 810      815 820      825 830      835 840      845 850
          *              *              *              *
AGTTTGTATC ACTTACTTGC AGCACACGCA TCCTTCCCTG CCTCACTATG
TCAAACTAG  TGAATGAACG TCGTGTGCGT AGGAAGGGAC GGAGTGATAC

    855 860      865 870      875 880      885 890      895 900
          *              *              *              *
ACTCGTCTGA GTGGGATTGG TTGAGGGGAG CTTTGGCCAC CGTTGACAGA
TGAGCAGACT CACCCTAACC AACTCCCCTC GAAACCGGTG GCAACTGTCT

    905 910      915 920      925 930      935 940      945 950
          *              *              *              *
GACTACGGAA TCTTGAACAA GGTCTTCCAC AATATCACGG ACACGCACGT
CTGATGCCTT AGAACTTGTT CCAGAAGGTG TTATAGTGCC TGTGCGTGCA

    955 960      965 970      975 980      985 990      995 1000
          *              *              *              *
GGCGCATCAC CTGTTCTCGA CCATGCCGCA TTATCATGCG ATGGAAGCTA
CCGCGTAGTG GACAAGAGCT GGTACGGCGT AATAGTACGC TACCTTCGAT

    1005 1010      1015 1020      1025 1030      1035 1040      1045 1050
          *              *              *              *
CGAAGGCGAT AAAGCCGATA CTGGGAGAGT ATTATCAGTT GCATGGGACG
GCTTCCGCTA TTTCGGCTAT GACCCTCTCA TAATAGTCAA CGTACCCTGC

    1055 1060      1065 1070      1075 1080      1085 1090      1095 1100
          *              *              *              *
CCGGTGGTTA AGGCGATGTG GAGGGAGGCG AAGGAGTGTA TCTATGTGGA
GGCCACCAAT TCCGCTACAC CTCCCTCCGC TTCCTCACAT AGATACACCT

    1105 1110      1115 1120      1125 1130      1135 1140      1145 1150
          *              *              *              *
ACCGGACAGG CAAGGTGAGA AGAAAGGTGT GTTCTGGTAC AACAAATAAGT
TGGCCTGTCC GTTCCACTCT TCTTTCCACA CAAGACCATG TTGTTATTCA

    1155 1160      1165 1170
          *              *
TATGAAGCAA AGAAGAAACA AT
ATACTTCGTT TCTTCTTTGT TA

```

Sequence Range: 1 to 1172

5	10	15	20	25	30	35	40	45							
	*		*		*		*								
ATG	GGT	GCA	GGT	GGA	AGA	ATG	CAA	GTG	TCT	CCT	CCC	TCC	AAA	AAG	TCT
TAC	CCA	CGT	CCA	CCT	TCT	TAC	GTT	CAC	AGA	GGA	GGG	AGG	TTT	TTC	AGA
M	G	A	G	G	R	M	Q	V	S	P	P	S	K	K	S>
50	55	60	65	70	75	80	85	90	95						
*		*		*		*		*							
GAA	ACC	GAC	AAC	ATC	AAG	CGC	GTA	CCC	TGC	GAG	ACA	CCG	CCC	TTC	ACT
CTT	TGG	CTG	TTG	TAG	TTC	GCG	CAT	GGG	ACG	CTC	TGT	GGC	GGG	AAG	TGA
E	T	D	N	I	K	R	V	P	C	E	T	P	P	F	T>
100	105	110	115	120	125	130	135	140							
*		*		*		*		*							
GTC	GGA	GAA	CTC	AAG	AAA	GCA	ATC	CCA	CCG	CAC	TGT	TTC	AAA	CGC	TCG
CAG	CCT	CTT	GAG	TTC	TTT	CGT	TAG	GGT	GGC	GTG	ACA	AAG	TTT	GCG	AGC
V	G	E	L	K	K	A	I	P	P	H	C	F	K	R	S>
145	150	155	160	165	170	175	180	185	190						
*	*		*		*		*		*						
ATC	CCT	CGC	TCT	TTC	TCC	TAC	CTC	ATC	TGG	GAC	ATC	ATC	ATA	GCC	TCC
TAG	GGA	GCG	AGA	AAG	AGG	ATG	GAG	TAG	ACC	CTG	TAG	TAG	TAT	CGG	AGG
I	P	R	S	F	S	Y	L	I	W	D	I	I	I	A	S>
195	200	205	210	215	220	225	230	235	240						
*	*		*		*		*		*						
TGC	TTC	TAC	TAC	GTC	GCC	ACC	ACT	TAC	TTC	CCT	CTC	CTC	CCT	CAC	CCT
ACG	AAG	ATG	ATG	CAG	CGG	TGG	TGA	ATG	AAG	GGA	GAG	GAG	GGA	GTG	GGA
C	F	Y	Y	V	A	T	T	Y	F	P	L	L	P	H	P>
245	250	255	260	265	270	275	280	285							
*	*		*		*		*								
CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAG	GGC	TGC	GTC
GAG	AGG	ATG	AAG	CGG	ACC	GGA	GAG	ATG	ACC	CGG	ACG	GTC	CCG	ACG	CAG
L	S	Y	F	A	W	P	L	Y	W	A	C	Q	G	C	V>
290	295	300	305	310	315	320	325	330	335						
*	*		*		*		*		*						
CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	GAG	TGC	GGC	CAC	CAC	GCC	TTC
GAT	TGG	CCG	CAG	ACC	CAG	TAT	CGG	GTG	CTC	ACG	CCG	GTG	GTG	CGG	AAG
L	T	G	V	W	V	I	A	H	<del>CTC</del>	C	G	H	H	A	F>
340	345	350	355	360	365	370	375	380							
*	*		*		*		*								
AGC	GAC	TAC	CAG	TGG	CTG	GAC	GAC	ACC	GTC	GGC	CTC	ATC	TTC	CAC	TCC
TCG	CTG	ATG	GTC	ACC	GAC	CTG	CTG	TGG	CAG	CCG	GAG	TAG	AAG	GTG	AGG
S	D	Y	Q	W	L	D	D	T	V	G	L	I	F	H	S>
385	390	395	400	405	410	415	420	425	430						
*	*		*		*		*		*						
TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGA	CGC	CAC
AAG	GAG	GAG	CAG	GGA	ATG	AAG	AGG	ACC	TTC	ATG	TCA	GTA	GCT	GCG	GTG
F	L	L	V	P	Y	F	S	W	K	Y	S	H	R	R	H>
435	440	445	450	455	460	465	470	475	480						
*	*		*		*		*		*						
CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG
GTA	AGG	TTG	TGA	CCG	AGG	GAG	CTC	TCT	CTG	CTT	CAC	AAA	CAG	GGG	TTC
H	S	N	T	G	S	L	E	R	D	E	V	F	V	P	K>

```

485   490   495   500   505   510   515   520   525
      *           *           *
AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CAC AAC AAC CCT TTG
TTC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GCG TTG TTG GGA AAC
K   K   S   D   I   K   W   Y   G   K   Y   N   N   P   L>

530   535   540   545   550   555   560   565   570   575
      *           *           *
GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG
CCT GCG TGG CAC TAC AAT TGC CAA GTC AAG TGA GAG CCG ACC GGA AAC
G   R   T   V   M   L   T   V   Q   F   T   L   G   W   P   L>

580   585   590   595   600   605   610   615   620
      *           *           *
TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT
ATG AAT CGG AAG TTG CAG AGC CCC TCT GGA ATG CTG CCG CCG AAG CGA
Y   L   A   F   N   V   S   G   R   P   Y   D   G   G   F   A>

625   630   635   640   645   650   655   660   665   670
      *           *           *
TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC
ACG GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG
C   H   F   H   P   N   A   P   I   Y   N   D   R   E   R   L>

675   680   685   690   695   700   705   710   715   720
      *           *           *
CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC
GTC TAT ATG TAG AGG CTG CGA CCG TAG GAG CGG CAG ACG ATG CCA GAG
Q   I   Y   I   S   D   A   G   I   L   A   V   C   Y   G   L>

725   730   735   740   745   750   755   760   765
      *           *           *
TAC CGC TAC GCT GCT GTC CAA GGA GTT GCC TCG ATG GTC TGC TTC TAC
ATG GCG ATG CGA CGA CAG GTT CCT CAA CGG AGC TAC CAG ACG AAG ATG
Y   R   Y   A   A   V   Q   G   V   A   S   M   V   C   F   Y>

770   775   780   785   790   795   800   805   810   815
      *           *           *
GGA GTT CCG CTT CTG ATT GTC AAT GGG TTC TTA GTT TTG ATC ACT TAC
CCT CAA GGC GAA GAC TAA CAG TTA CCC AAG AAT CAA AAC TAG TGA ATG
G   V   P   L   L   I   V   N   G   F   L   V   L   I   T   Y>

820   825   830   835   840   845   850   855   860
      *           *           *
TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG TCT GAG TGG
AAC GTC GTG TGC GTA GGA AGG GAC GGA GTG ATA CTG AGC AGA CTC ACC
L   Q   H   T   H   P   S   L   P   H   Y   D   S   S   E   W>

865   870   875   880   885   890   895   900   905   910
      *           *           *
GAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC TAC GGA ATC
CTA ACC AAC TCC CCT CGA AAC CGG TGG CAA CTG TCT CTG ATG CCT TAG
D   W   L   R   G   A   L   A   T   V   D   R   D   Y   G   I>

915   920   925   930   935   940   945   950   955   960
      *           *           *
TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG GCG CAT CAC
AAC TTG TTC CAG AAG GTG TTA TAG TGC CTG TGC GTG CAC CGC GTA GTG
L   N   K   V   F   H   N   I   T   D   T   H   V   A   H   H>

965   970   975   980   985   990   995   1000   1005
      *           *           *

```

```

CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT ACG AAG GCG
GAC AAG AGC TGG TAC GGC GTA ATA GTA CGC TAC CTT CGA TGC TTC CGC
  L   F   S   T   M   P   H   Y   H   A   M   E   A   T   K   A>

1010   1015   1020   1025   1030   1035   1040   1045   1050   1055
  *           *           *           *           *
ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTG CAT GGG ACG CCG GTG
TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAC GTA CCC TGC GGC CAC
  I   K   P   I   L   G   E   Y   Y   Q   L   H   G   T   P   V>

1060   1065   1070   1075   1080   1085   1090   1095   1100
  *           *           *           *           *
GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG
CAA TTC CGC TAC ACC TCC CTC CGC TTC CTC ACA TAG ATA CAC CTT GGC
  V   K   A   M   W   R   E   A   K   E   C   I   Y   V   E   P>

1105   1110   1115   1120   1125   1130   1135   1140   1145   1150
  *           *           *           *           *
GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA
CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT
  D   R   Q   G   E   K   K   G   V   F   W   Y   N   N   K   L>

1155   1160   1165   1170
  *           *
TGA AGC AAA GAA GAA ACA AT
ACT TCG TTT CTT CTT TGT TA
  *   S   K   E   E   T   X>

```

5	10	15	20	25	30	35	40	45	50
	*		*		*		*		*
ATGGGTGCAG	GTGGAAGAAT	GCAAGTGTCT	CCTCCCTCCA	AGAAGTCTGA					
TACCCACGTC	CACCTTCTTA	CGTTCACAGA	GGAGGGAGGT	TCTTCAGACT					
55	60	65	70	75	80	85	90	95	100
	*		*		*		*		*
AACCGACACC	ATCAAGCGCG	TACCCTGCGA	GACACCGCCC	TTCAGTGTCTG					
TTGGCTGTGG	TAGTTCGCGC	ATGGGACGCT	CTGTGGCGGG	AAGTGACAGC					
105	110	115	120	125	130	135	140	145	150
	*		*		*		*		*
GAGAACTCAA	GAAAGCAATC	CCACCGCACT	GTTTCAAACG	CTCGATCCCT					
CTCTTGAGTT	CTTTCGTTAG	GGTGGCGTGA	CAAAGTTTGC	GAGCTAGGGA					
155	160	165	170	175	180	185	190	195	200
	*		*		*		*		*
CGCTCTTTCT	CCTACCTCAT	CTGGGACATC	ATCATAGCCT	CCTGCTTCTA					
GCGAGAAAGA	GGATGGAGTA	GACCCTGTAG	TAGTATCGGA	GGACGAAGAT					
205	210	215	220	225	230	235	240	245	250
	*		*		*		*		*
CTACNTCGCC	ACCACCTTACT	TCCCTCTCCT	CCCTCACCCCT	CTCTCCTACT					
GATGNAGCGG	TGGTGAATGA	AGGGAGAGGA	GGGAGTGGGA	GAGAGGATGA					
255	260	265	270	275	280	285	290	295	300
	*		*		*		*		*
TCGCCTGGCC	TCTCTACTGG	GCCTGCCAAG	GGTGCGTCCT	AACCGGCGTC					
AGCGGACCGG	AGAGATGACC	CGGACGGTTC	CCACGCAGGA	TTGGCCGCGG					
305	310	315	320	325	330	335	340	345	350
	*		*		*		*		*
TGGGTCATAG	CCCACAGTGT	CGGCCACCAC	GCCTTCAGCG	ACTACCACTG					
ACCCAGTATC	GGGTGATCAC	GCCGGTGGTG	CGGAAGTCGC	TGATGGTCAC					
355	360	365	370	375	380	385	390	395	400
	*		*		*		*		*
GCTTGACGAC	ACCGTCGGTC	TCATCTTCCA	CTCCTTCCTC	CTCGTCCCTT					
CGAACTGCTG	TGGCAGCCAG	AGTAGAAGGT	GAGGAAGGAG	GAGCAGGGAA					
405	410	415	420	425	430	435	440	445	450
	*		*		*		*		*
ACTTCTCCTG	GAAGTACAGT	CATCGCAGCC	ACCATTCCAA	CACTGGCTCC					
TGAAGAGGAC	CTTCATGTCA	GTAGCGTCGG	TGGTAAGGTT	GTGACCGAGG					
455	460	465	470	475	480	485	490	495	500
	*		*		*		*		*
CTCGAGAGAG	ACGAAGTGTT	TGTCCCAAG	AAGAAGTCAG	ACATCAAGTG					
GAGCTCTCTC	TGCTTCACAA	ACAGGGGTTC	TTCTTCAGTC	TGTAGTTTAC					
505	510	515	520	525	530	535	540	545	550
	*		*		*		*		*
GTACGGCAAG	TACCTCAACA	ACCCTTTGGG	ACGCACCGTG	ATGTTAACGG					
CATGCCGTTC	ATGGAGTTGT	TGGGAAACCC	TGCGTGGCAC	TACAATTGCC					
555	560	565	570	575	580	585	590	595	600
	*		*		*		*		*
TTCAGTTTAC	TCTCGGCTGG	CCGTTGTACT	TAGCCTTCAA	CGTCTCGGGA					
AAGTCAAGTG	AGAGCCGACC	GGCAACATGA	ATCGGAAGTT	GCAGAGCCCT					
605	610	615	620	625	630	635	640	645	650
	*		*		*		*		*
AGACCTTACG	ACGGCGGCTT	CCGTTGCCAT	TTCCACCCCA	ACGCTCCCAT					

G (in wild type D gene)

```

TCTGGAATGC TGCCGCCGAA GGCAACGGTA AAGGTGGGGT TGCGAGGGTA
    655  660    665  670    675  680    685  690    695  700
          *          *          *          *
CTACAACGAC CGCGAGCGTC TCCAGATATA CATCTCCGAC GCTGGCATCC
GATGTTGCTG GCGCTCGCAG AGGTCTATAT GTAGAGGCTG CGACCGTAGG

    705  710    715  720    725  730    735  740    745  750
          *          *          *          *
TCGCCGTCTG CTACGGTCTC TTCCGTTACG CCGCCGGCCA GGGAGTGGCC
AGCGGCAGAC GATGCCAGAG AAGGCAATGC GGCGGCCGGT CCCTCACCGG

    755  760    765  770    775  780    785  790    795  800
          *          *          *          *
TCGATGGTCT GCTTCTACGG AGTCCCGCTT CTGATTGTCA ATGGTTTCCT
AGCTACCAGA CGAAGATGCC TCAGGGCGAA GACTAACAGT TACCAAAGGA

    805  810    815  820    825  830    835  840    845  850
          *          *          *          *
CGTGTTGATC ACTTACTTGC AGCACACGCA TCCTTCCCTG CCTCACTACG
GCACAAC TAGAATGAACG TCGTGTGCGT AGGAAGGGAC GGAGTGATGC

    855  860    865  870    875  880    885  890    895  900
          *          *          *          *
ATTTCGTCCGA GTGGGATTGG TTCAGGGGAG CTTTGGCTAC CGTTGACAGA
TAAGCAGGCT CACCCTAACC AAGTCCCCTC GAAACCGATG GCAACTGTCT

    905  910    915  920    925  930    935  940    945  950
          *          *          *          *
GACTACGGAA TCTTGAACAA GGTCTTCCAC AATATTACCG ACACGCACGT
CTGATGCCTT AGAACTTGTT CCAGAAGGTG TTATAATGGC TGTGCGTGCA

    955  960    965  970    975  980    985  990    995 1000
          *          *          *          *
GGCCCATCAT CCGTTCTCCA CGATGCCGCA TTATCACGCG ATGGAAGCTA
CCGGGTAGTA GGCAAGAGGT GCTACGGCGT AATAGTGCGC TACCTTCGAT

    1005 1010    1015 1020    1025 1030    1035 1040    1045 1050
          *          *          *          *
CCAAGGCGAT AAAGCCGATA CTGGGAGAGT ATTATCAGTT CGATGGGACG
GGTTCCGCTA TTTCGGCTAT GACCCTCTCA TAATAGTCAA GCTACCCTGC

    1055 1060    1065 1070    1075 1080    1085 1090    1095 1100
          *          *          *          *
CCGGTGGTTA AGGCGATGTG GAGGGAGGCG AAGGAGTGTA TCTATGTGGA
GGCCACCAAT TCCGCTACAC CTCCCTCCGC TTCCTCACAT AGATACACCT

    1105 1110    1115 1120    1125 1130    1135 1140    1145 1150
          *          *          *          *
ACCGGACAGG CAAGGTGAGA AGAAAGGTGT GTTCTGGTAC AACAATAAGT
TGGCCTGTCC GTTCCA CTCTTCCACA CAAGACCATG TTGTTATTCA

    1155 1160    1165 1170    1175 1180    1185
          *          *          *
TATGAGGATA TGATGATGGT GAAAGAAATC ACTAG
ATACTCCTAT ACTACTACCA CTTTCTTTAG TGATC

```

Sequence Range: 1 to 1185

5	10	15	20	25	30	35	40	45
	*		*		*		*	
ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT								
TAC CCA CGT CCA CCT TCT TAC GTT CAC AGA GGA GGG AGG TTC TTC AGA								
M G A G G R M Q V S P P S K K S>								
50	55	60	65	70	75	80	85	90
*		*		*		*		*
GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT								
CTT TGG CTG TGG TAG TTC GCG CAT GGG ACG CTC TGT GGC GGG AAG TGA								
E T D T I K R V P C E T P P F T>								
100	105	110	115	120	125	130	135	140
*		*		*		*		*
GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG								
CAG CCT CTT GAG TTC TTT CGT TAG GGT GGC GTG ACA AAG TTT GCG AGC								
V G E L K K A I P P H C F K R S>								
145	150	155	160	165	170	175	180	185
	*		*		*		*	
ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC								
TAG GGA GCG AGA AAG AGG ATG GAG TAG ACC CTG TAG TAG TAT CGG AGG								
I P R S F S Y L I W D I I I A S>								
195	200	205	210	215	220	225	230	235
	*		*		*		*	
TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT								
ACG AAG ATG ATG NAG CGG TGG TGA ATG AAG GGA GAG GAG GGA GTG GGA								
C F Y Y X A T T Y F P L L P H P>								
245	250	255	260	265	270	275	280	285
	*		*		*		*	
CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC								
GAG AGG ATG AAG CGG ACC GGA GAG ATG ACC CGG ACG GTT CCC ACG CAG								
L S Y F A W P L Y W A C Q G C V>								
290	295	300	305	310	315	320	325	330
*		*		*		*		*
CTA ACC GGC GTC TGG GTC ATA GCC CAC AAG TGC GGC CAC CAC GCC TTC								
GAT TGG CCG CAG ACC CAG TAT CGG GTG TTC ACG CCG GTG GTG CGG AAG								
L T G V W V I A H <del>ATC</del> C G H H A F>								
340	345	350	355	360	365	370	375	380
*		*		*		*		*
AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC								
TCG CTG ATG GTC ACC GAA CTG CTG TGG CAG CCA GAG TAG AAG GTG AGG								
S D Y Q W L D D T V G L I F H S>								
385	390	395	400	405	410	415	420	425
	*		*		*		*	
TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC								
AAG GAG GAG CAG GGA ATG AAG AGG ACC TTC ATG TCA GTA GCG TCG GTG								
F L L V P Y F S W K Y S H R S H>								
435	440	445	450	455	460	465	470	475
	*		*		*		*	
CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG								
GTA AGG TTG TGA CCG AGG GAG CTC TCT CTG CTT CAC AAA CAG GGG TTC								
H S N T G S L E R D E V F V P K>								



```

    485      490      495      500      505      510      515      520      525
          *          *          *          *          *
AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG
TTC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GAG TTG TTG GGA AAC
K   K   S   D   I   K   W   Y   G   K   Y   L   N   N   P   L>

530      535      540      545      550      555      560      565      570      575
          *          *          *          *          *
GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG
CCT GCG TGG CAC TAC AAT TGC CAA GTC AAG TGA GAG CCG ACC GGC AAC
G   R   T   V   M   L   T   V   Q   F   T   L   G   W   P   L>

    580      585      590      595      600      605      610      615      620
          *          *          *          *          *
TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT
ATG AAT CGG AAG TTG CAG AGC CCT TCT GGA ATG CTG CCG CCG AAG GCA
Y   L   A   F   N   V   S   G   R   P   Y   D   G   G   F   R>

625      630      635      640      645      650      655      660      665      670
          *          *          *          *          *
TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC
ACG GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG
C   H   F   H   P   N   A   P   I   Y   N   D   R   E   R   L>

675      680      685      690      695      700      705      710      715      720
          *          *          *          *          *
CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC
GTC TAT ATG TAG AGG CTG CGA CCG TAG GAG CGG CAG ACG ATG CCA GAG
Q   I   Y   I   S   D   A   G   I   L   A   V   C   Y   G   L>

    725      730      735      740      745      750      755      760      765
          *          *          *          *          *
TTC CGT TAC GCC GCC GGC CAG GGA GTG GCC TCG ATG GTC TGC TTC TAC
AAG GCA ATG CGG CGG CCG GTC CCT CAC CGG AGC TAC CAG ACG AAG ATG
F   R   Y   A   A   G   Q   G   V   A   S   M   V   C   F   Y>

770      775      780      785      790      795      800      805      810      815
          *          *          *          *          *
GGA GTC CCG CTT CTG ATT GTC AAT GGT TTC CTC GTG TTG ATC ACT TAC
CCT CAG GGC GAA GAC TAA CAG TTA CCA AAG GAG CAC AAC TAG TGA ATG
G   V   P   L   L   I   V   N   G   F   L   V   L   I   T   Y>

    820      825      830      835      840      845      850      855      860
          *          *          *          *          *
TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG
AAC GTC GTG TGC GTA GGA AGG GAC GGA GTG ATG CTA AGC AGG CTC ACC
L   Q   H   T   H   P   S   L   P   H   Y   D   S   S   E   W>

865      870      875      880      885      890      895      900      905      910
          *          *          *          *          *
GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC
CTA ACC AAG TCC CCT CGA AAC CGA TGG CAA CTG TCT CTG ATG CCT TAG
D   W   F   R   G   A   L   A   T   V   D   R   D   Y   G   I>

915      920      925      930      935      940      945      950      955      960
          *          *          *          *          *
TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT
AAC TTG TTC CAG AAG GTG TTA TAA TGG CTG TGC GTG CAC CGG GTA GTA
L   N   K   V   F   H   N   I   T   D   T   H   V   A   H   H>

    965      970      975      980      985      990      995      1000      1005
          *          *          *          *          *

```

CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG  
GGC AAG AGG TGC TAC GGC GTA ATA GTG CGC TAC CTT CGA TGG TTC CGC  
P F S T M P H Y H A M E A T K A>

1010 1015 1020 1025 1030 1035 1040 1045 1050 1055  
\* \* \* \*

ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG  
TAT TTC GGC TAT GAC CCT CTC ATA ATA GTG AAG CTA CCC TGC GGC CAC  
I K P I L G E Y Y Q F D G T P V>

1060 1065 1070 1075 1080 1085 1090 1095 1100  
\* \* \* \*

GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG  
CAA TTC CGC TAC ACC TCC CTC CGC TTC CTC ACA TAG ATA CAC CTT GGC  
V K A M W R E A K E C I Y V E P>

1105 1110 1115 1120 1125 1130 1135 1140 1145 1150  
\* \* \* \*

GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA  
CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT  
D R Q G E K K G V F W Y N N K L>

1155 1160 1165 1170 1175 1180 1185  
\* \* \*

TGA GGA TAT GAT GAT GGT GAA AGA AAT CAC TAG  
ACT CCT ATA CTA CTA CCA CTT TCT TTA GTG ATC  
\* G Y D D G E R N H \*>